

Pathoscope Initial Analysis

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Objective: Approach:

Loading Data

```
library(knitr)
library(ggplot2)
library(outliers)
source('gather_pathoscope.R')
```

```
##
## Attaching package: 'dplyr'
##
## The following objects are masked from 'package:plyr':
##
##   arrange, count, desc, failwith, id, mutate, rename, summarise,
##   summarize
##
## The following object is masked from 'package:stats':
##
##   filter
##
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union
##
## Loading required package: reshape2
```

```
## Warning in readLines(inputfile): incomplete final line found on
## '../../bioinf/genome_purity/RM8375_pathoscope_pipeline_params.txt'
```

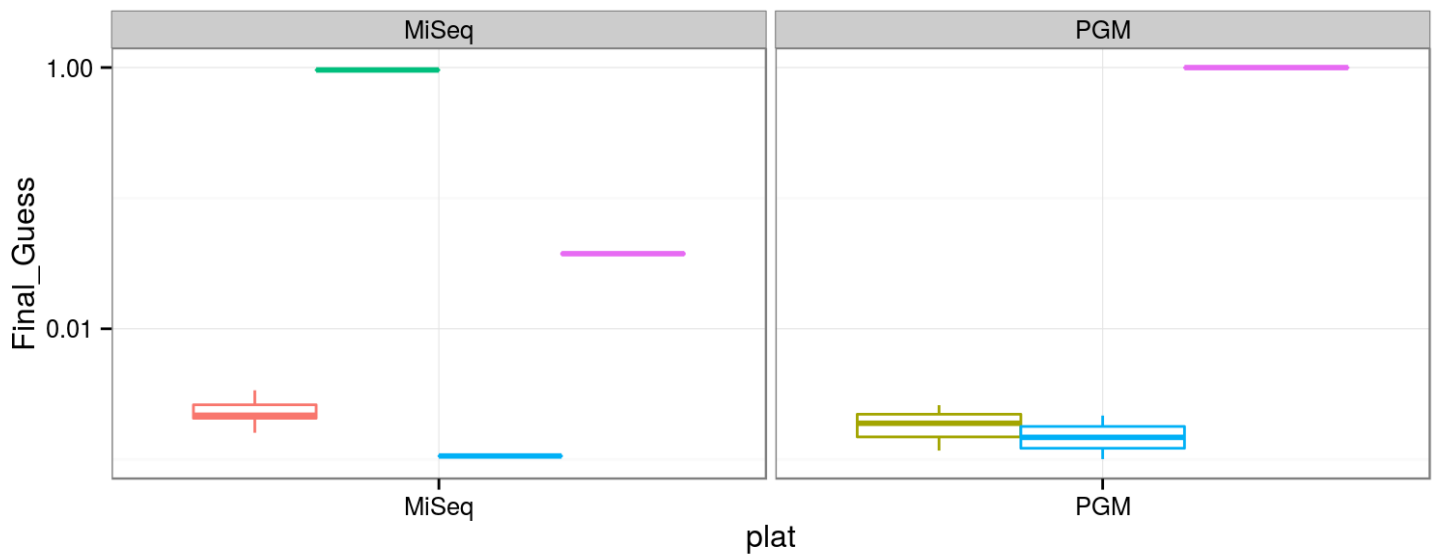
```
df <- join(pathoDF, sampleDF)
```

```
## Joining by: filename
```

Top matches

The organisms with the top matches were all *Salmonella enterica subspecies enterica*, and the porportion of reads assigned to the top matches was statistically similiar for all replicates (library, and vials).

```
ggplot(df[df$Final_Guess > 0.001,]) + geom_boxplot(aes(y = Final_Guess, x = plat, color = Genome)) + scale_y_log10() + facet_wrap(~plat, scale = "free_x") + theme_bw() + theme(legend.position = "bottom", legend.direction = "vertical")
```



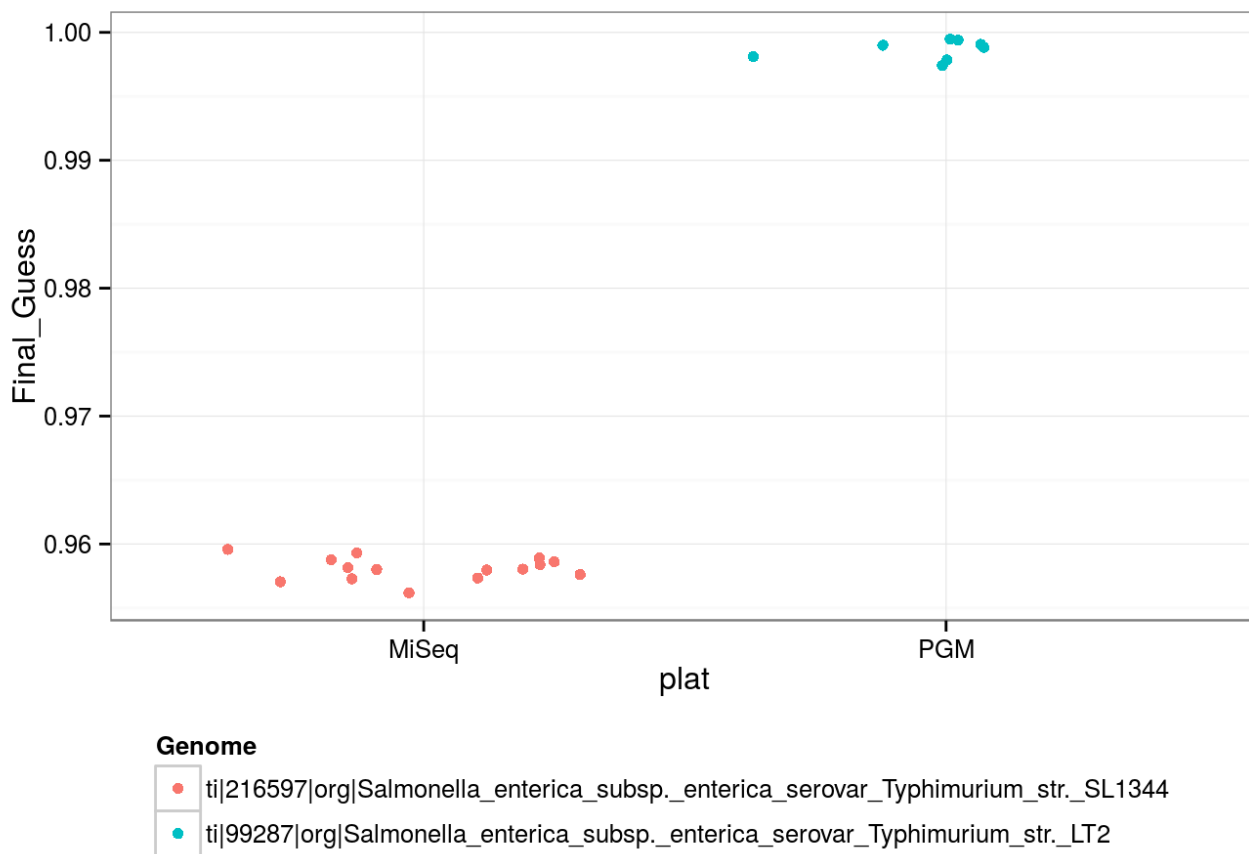
Genome

- ti|1081093|org|Salmonella_enterica_subsp._enterica_serovar_Gallinarum/pullorum
- ti|1171376|org|Salmonella_enterica_subsp._enterica_serovar_Typhimurium_str._U288
- ti|216597|org|Salmonella_enterica_subsp._enterica_serovar_Typhimurium_str._SL1344
- ti|718274|org|Salmonella_enterica_subsp._enterica_serovar_Typhimurium_str.
- ti|99287|org|Salmonella_enterica_subsp._enterica_serovar_Typhimurium_str._LT2

Top proportion of assignments for all datasets were correct to the subspecies level. LT2 was the top portion for all PGM datasets but not for MiSeq.

Top Assignment Repeatability

```
ggplot(df[df$Final_Guess > 0.1,]) + geom_jitter(aes(y = Final_Guess, x = plat, color = Genome)) + theme_bw() + theme(legend.position = "bottom", legend.direction = "vertical")
```



None of the predicted proportion values for the top hit for the sequencing platforms are outliers.

```
for(i in c("MiSeq", "PGM")){
  print(i)
  print(dixon.test(df$Final_Guess[df$Final_Guess > 0.1 & df$plat == i]))
}
```

```
## [1] "MiSeq"
##
## Dixon test for outliers
##
## data: df$Final_Guess[df$Final_Guess > 0.1 & df$plat == i]
## Q = 0.3999, p-value = 0.4077
## alternative hypothesis: lowest value 0.956187068637446 is an outlier
##
## [1] "PGM"
##
## Dixon test for outliers
##
## data: df$Final_Guess[df$Final_Guess > 0.1 & df$plat == i]
## Q = 0.2187, p-value = 0.9636
## alternative hypothesis: lowest value 0.997400615184494 is an outlier
```

Proportion of Salmonella

Contaminants defined as any reads not taxonomically classified as *Salmonella*, the genus level cutoff is based on prior analysis of results pairwise mixtures of simulated reads from seven different organisms.

```
df$Contam <- !(grepl("Salmonella", df$Genome))
```

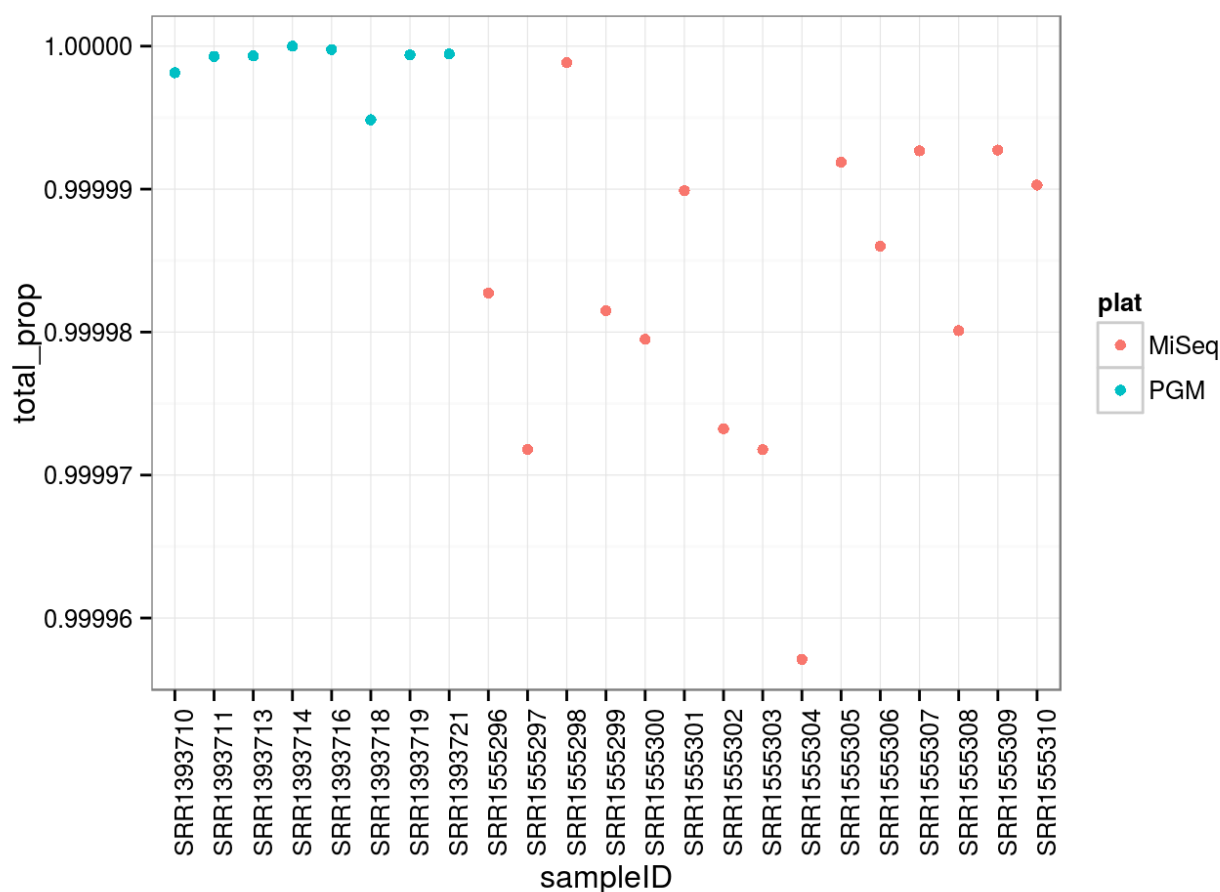
Total proportion of **Salomonella** reads

```
df_salmonella <- df[df$Contam == FALSE,] %>% ddply(.variables = .(sampleID, plat), summarize, total_prop = sum(Final_Guess))
```

Note that there are only 23 datasets, one missing MiSeq

Comparison of Total Salmonella by dataset.

```
ggplot(df_salmonella) + geom_point(aes(x = sampleID, y = total_prop, color = plat)) + theme_bw() + theme(axis.text.x = element_text(angle = 90))
```



Comparison of total proportions by platform

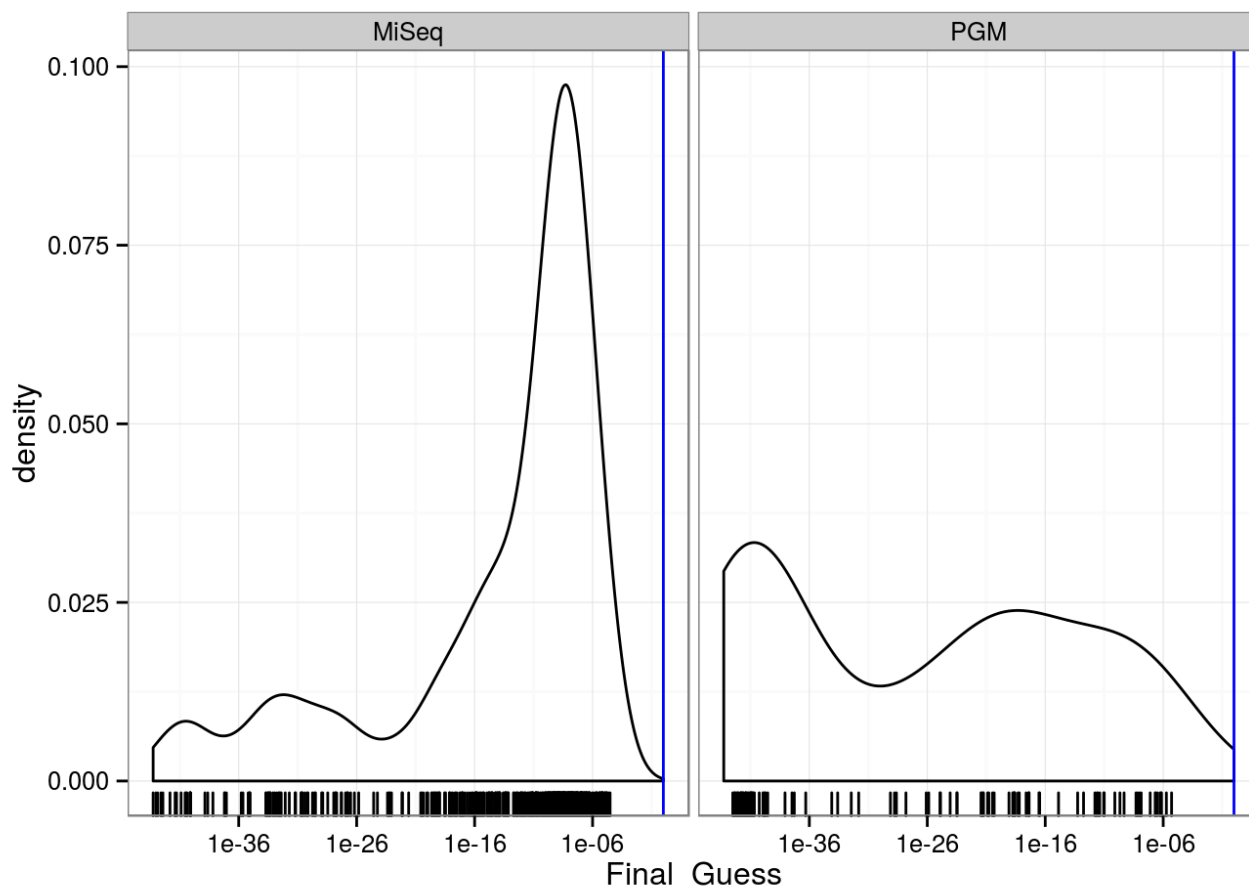
```
t.test(x = df_salmonella$total_prop[df_salmonella$plat == "PGM"], y = df_salmonella$total_prop[df_salmonella$plat == "MiSeq"])
```

```
##
## Welch Two Sample t-test
##
## data: df_salmonella$total_prop[df_salmonella$plat == "PGM"] and df_salmonella$total_prop[df_salmonella$plat == "MiSeq"]
## t = 5.5948, df = 15.206, p-value = 4.863e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  9.976569e-06 2.223303e-05
## sample estimates:
## mean of x mean of y
## 0.9999988 0.9999827
```

Analysis of contaminants

Defining contaminants as non-*Salmonella*, sequence purity and genomic structure analysis are better suited for evaluating the presence of closely related species within the material.

```
ggplot(df[df$Contam == TRUE,]) + geom_density(aes(x = Final_Guess), alpha = 0.25) + geom_rug(aes(x = Final_Guess)) + facet_wrap(~plat) + geom_vline(aes(xintercept = 1), color = "blue") + scale_x_log10() + theme_bw()
```



Blue vertical line, at 1 to serve as a reference point.

Contaminant Summary

```
df_contam <- ddply(df[df$Contam == TRUE,],.variables = .(Genome, plat),summarize, median=median(Final_Guess), max=max(Final_Guess),min=min(Final_Guess)) %>% arrange(desc(median))
```

Genome	plat	median	max	min
ti 32630 org synthetic_construct	MiSeq	1.11614e-05	3.03505e-05	0.0000e+00
ti 696406 org Escherichia_coli_UMNK88	MiSeq	5.86550e-06	5.86550e-06	5.8655e-06
ti 481805 org Escherichia_coli_ATCC_8739	MiSeq	3.83970e-06	7.85370e-06	9.0400e-08
ti 300268 org Shigella_boydii_Sb227	MiSeq	2.50030e-06	2.50030e-06	2.5003e-06
ti 585055 org Escherichia_coli_55989	PGM	9.28000e-07	1.85610e-06	0.0000e+00
ti 536056 org Escherichia_coli_DH1	PGM	6.59700e-07	5.14650e-06	0.0000e+00
ti 1246486 org synthetic_Enterobacteria_phage_phiX174.1f	MiSeq	5.83700e-07	1.16730e-06	0.0000e+00
ti 266264 org Cupriavidus_metallidurans_CH34	MiSeq	3.15600e-07	3.15600e-07	3.1560e-07
ti 910348 org Escherichia_coli_P12b	MiSeq	2.85800e-07	1.17958e-05	4.9000e-09
ti 331112 org Escherichia_coli_HS	PGM	2.81400e-07	3.28100e-07	2.3480e-07
ti 1028764 org Cloning_vector_HPdO	MiSeq	2.67000e-07	5.34000e-07	0.0000e+00
ti 1218933 org Pectobacterium_carotovorum_subsp.carotovorumPCC21	MiSeq	1.43400e-07	2.86700e-07	0.0000e+00
ti 10847 org Enterobacteria_phage_phiX174	MiSeq	1.37300e-07	4.28380e-06	0.0000e+00
ti 274589 org VCSM13_interference-resistant_helper_phage	MiSeq	1.23700e-07	5.34000e-07	0.0000e+00
ti 0 org Unknown.	MiSeq	1.18000e-07	5.64700e-07	4.6000e-09
ti 693216 org Cronobacter_turicensis_z3032	MiSeq	9.92000e-08	9.92000e-08	9.9200e-08
ti 585054 org Escherichia_fergusonii_ATCC_35469	MiSeq	6.20000e-08	1.24100e-07	0.0000e+00
ti 926017 org VCSM13_AviTag-pVII_modified_interference-resistant_helper_phage	MiSeq	6.18000e-08	1.23700e-07	0.0000e+00
ti 926018 org VCSM13_FLAG-pVII_modified_interference-resistant_helper_phage	MiSeq	6.18000e-08	1.23700e-07	0.0000e+00
ti 926019 org VCSM13_HIS6-pVII_modified_interference-resistant_helper_phage	MiSeq	6.18000e-08	1.23700e-07	0.0000e+00
ti 1045856 org Enterobacter_cloacae_EcWSU1	MiSeq	5.27000e-08	1.09300e-07	3.5000e-09
ti 507522 org Klebsiella_pneumoniae_342	MiSeq	5.01000e-08	5.02000e-08	5.0000e-08

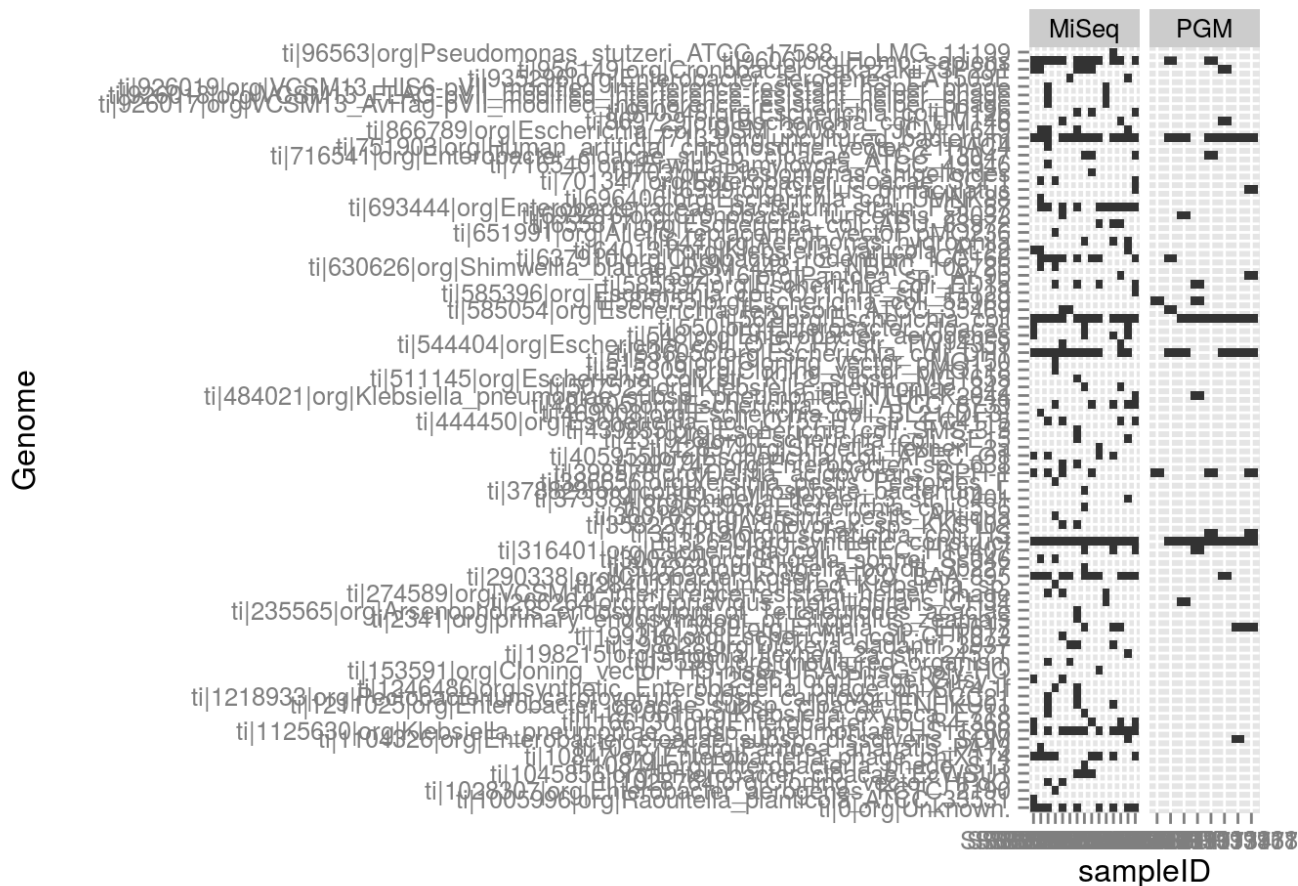
ti 511145 org Escherichia_coli_str.K-12substr._MG1655	MiSeq	4.93000e-08	4.93000e-08	4.9300e-08
ti 751903 org Human_artificial_chromosome_vector_21HAC4	MiSeq	4.58000e-08	4.58000e-08	4.5800e-08
ti 215689 org Erwinia_sp._Ejp617	MiSeq	4.35000e-08	1.95800e-07	0.0000e+00
ti 2341 org primary_endosymbiont_of_Sitophilus_zeamais	MiSeq	3.83000e-08	3.83000e-08	3.8300e-08
ti 536056 org Escherichia_coli_DH1	MiSeq	3.46000e-08	7.25270e-06	0.0000e+00
ti 10844 org Enterobacteria_phage_S13	MiSeq	3.32000e-08	3.32000e-08	3.3200e-08
ti 129861 org Phage_Gifsy-1	MiSeq	2.75000e-08	3.55000e-08	1.9500e-08
ti 439855 org Escherichia_coli_SMS-3-5	MiSeq	2.53000e-08	2.53000e-08	2.5300e-08
ti 550 org Enterobacter_cloacae	MiSeq	2.44000e-08	6.23000e-08	0.0000e+00
ti 362663 org Escherichia_coli_536	MiSeq	2.24000e-08	2.24000e-08	2.2400e-08
ti 544404 org Escherichia_coli_O157:H7_str._TW14359	MiSeq	2.10000e-08	2.63000e-08	1.5600e-08
ti 378823 org cotton_phyllosphere_bacterium_L	MiSeq	1.85000e-08	1.85000e-08	1.8500e-08
ti 1125630 org Klebsiella_pneumoniae_subsp.pneumoniaeHS11286	MiSeq	1.71000e-08	1.97800e-07	7.0000e-10
ti 153591 org Cloning_vector_HO-hisG-URA3-hisG-poly-HO	MiSeq	1.26000e-08	1.26000e-08	1.2600e-08
ti 866789 org Escherichia_coli_DSM_30083_=JCM1649	MiSeq	1.06000e-08	5.22000e-08	0.0000e+00
ti 199310 org Escherichia_coli_CFT073	MiSeq	9.80000e-09	9.80000e-09	9.8000e-09
ti 701347 org Enterobacter_cloacae_SCF1	MiSeq	9.30000e-09	1.55000e-08	1.7000e-09
ti 1211025 org Enterobacter_cloacae_subsp.cloacaeENHKU01	MiSeq	9.20000e-09	5.56000e-08	3.7000e-09
ti 693444 org Enterobacteriaceae_bacterium_strain_FGI_57	MiSeq	8.80000e-09	1.51200e-07	0.0000e+00
ti 956149 org Cronobacter_sakazakii_SP291	MiSeq	8.60000e-09	2.13000e-08	5.0000e-10
ti 1191061 org Klebsiella_oxytoca_E718	MiSeq	7.50000e-09	1.50000e-08	0.0000e+00
ti 644 org Aeromonas_hydrophila	MiSeq	5.80000e-09	5.18200e-07	0.0000e+00
ti 155900 org uncultured_organism	MiSeq	5.80000e-09	9.50000e-09	2.1000e-09
ti 42897 org Shigella_flexneri_2a	MiSeq	4.90000e-09	4.90000e-09	4.9000e-09
ti 9606 org Homo_sapiens	PGM	4.90000e-	9.70000e-	0.0000e+00

ti 399742 org Enterobacter_sp._638	MiSeq	4.40000e-09	8.70000e-09	0.0000e+00
ti 935296 org Enterobacter_aerogenes_EA1509E	MiSeq	4.00000e-09	7.30000e-09	6.0000e-10
ti 515309 org Cloning_vector_pMQ118	MiSeq	3.70000e-09	3.70000e-09	3.7000e-09
ti 515316 org Cloning_vector_pMQ150	MiSeq	3.70000e-09	3.70000e-09	3.7000e-09
ti 651991 org Allelic_replacement_vector_pMQ236	MiSeq	3.70000e-09	3.70000e-09	3.7000e-09
ti 484021 org Klebsiella_pneumoniae_subsp.pneumoniaeNTUH-K2044	MiSeq	3.70000e-09	3.70000e-09	3.7000e-09
ti 637910 org Citrobacter_rodentium_ICC168	MiSeq	3.70000e-09	2.57300e-07	5.0000e-10
ti 284011 org uncultured_Klebsiella_sp.	MiSeq	3.10000e-09	3.10000e-09	3.1000e-09
ti 585396 org Escherichia_coli_O111:H-str.11128	MiSeq	2.80000e-09	2.80000e-09	2.8000e-09
ti 592316 org Pantoea_sp._At-9b	MiSeq	2.50000e-09	2.50000e-09	2.5000e-09
ti 398578 org Delftia_acidovorans_SPH-1	MiSeq	2.20000e-09	2.69000e-08	0.0000e+00
ti 373384 org Shigella_flexneri_5_str._8401	MiSeq	2.10000e-09	2.10000e-09	2.1000e-09
ti 1166130 org Enterobacter_sp._R4-368	MiSeq	1.90000e-09	6.70000e-09	5.0000e-10
ti 77133 org uncultured_bacterium	MiSeq	1.60000e-09	6.99290e-06	0.0000e+00
ti 300269 org Shigella_sonnei_Ss046	MiSeq	1.50000e-09	2.90000e-09	0.0000e+00
ti 562 org Escherichia_coli	MiSeq	1.40000e-09	2.25490e-06	0.0000e+00
ti 585397 org Escherichia_coli_ED1a	MiSeq	1.30000e-09	5.77210e-06	0.0000e+00
ti 716541 org Enterobacter_cloacae_subsp.cloacaeATCC_13047	MiSeq	1.20000e-09	3.31000e-07	1.0000e-10
ti 1028307 org Enterobacter_aerogenes_KCTC_2190	MiSeq	1.20000e-09	1.20000e-09	1.2000e-09
ti 630626 org Shimwellia_blattae_DSM_4481_=NBRC105725	MiSeq	1.10000e-09	1.80000e-09	4.0000e-10
ti 1104326 org Enterobacter_cloacae_subsp.dissolvensSDM	MiSeq	1.10000e-09	1.10000e-09	1.1000e-09
ti 6999 org Gryllus_bimaculatus	MiSeq	1.00000e-09	1.00000e-09	1.0000e-09
ti 360102 org Yersinia_pestis_Antiqua	MiSeq	9.00000e-10	9.00000e-10	9.0000e-10
ti 290338 org Citrobacter_koseri_ATCC_BAA-895	MiSeq	9.00000e-10	8.27000e-08	0.0000e+00

ti 548 org Enterobacter_aerogenes	MiSeq	9.00000e-10	2.10000e-09	0.0000e+00
ti 405955 org Escherichia_coli_APEC_O1	MiSeq	8.00000e-10	4.80000e-09	0.0000e+00
ti 198628 org Dickeya_dadantii_3937	MiSeq	8.00000e-10	3.10000e-09	0.0000e+00
ti 869729 org Escherichia_coli_UM146	MiSeq	8.00000e-10	1.60000e-09	0.0000e+00
ti 716540 org Erwinia_amylovora_ATCC_49946	MiSeq	6.00000e-10	6.00000e-10	6.0000e-10
ti 640131 org Klebsiella_variicola_At-22	MiSeq	5.00000e-10	1.00000e-09	0.0000e+00
ti 32630 org synthetic_construct	PGM	5.00000e-10	2.09500e-07	0.0000e+00
ti 235565 org Arsenophonus_endosymbiont_of_Tetraleurodes_acaciae	MiSeq	5.00000e-10	5.00000e-10	5.0000e-10
ti 198215 org Shigella_flexneri_2a_str._2457T	MiSeq	4.00000e-10	4.00000e-10	4.0000e-10
ti 703 org Plesiomonas_shigelloides	MiSeq	4.00000e-10	4.00000e-10	4.0000e-10
ti 655817 org Escherichia_coli_ABU_83972	MiSeq	3.00000e-10	3.00000e-10	1.0000e-10
ti 431946 org Escherichia_coli_SE15	MiSeq	3.00000e-10	5.00000e-10	0.0000e+00
ti 358220 org Acidovorax_sp._KKS102	MiSeq	2.00000e-10	5.00000e-10	0.0000e+00
ti 1095774 org Pantoea_ananatis_PA13	MiSeq	2.00000e-10	2.00000e-10	2.0000e-10
ti 96563 org Pseudomonas_stutzeri_ATCC_17588_=LMG11199	MiSeq	2.00000e-10	2.00000e-10	2.0000e-10
ti 444450 org Escherichia_coli_O157:H7_str._EC4115	MiSeq	1.00000e-10	4.00000e-10	0.0000e+00
ti 1005996 org Raoultella_planticola_ATCC_33531	MiSeq	1.00000e-10	1.00000e-10	1.0000e-10
ti 386656 org Yersinia_pestis_Pestoides_F	MiSeq	1.00000e-10	1.00000e-10	1.0000e-10
ti 469008 org Escherichia_coli_BL21(DE3)	MiSeq	1.00000e-10	1.00000e-10	1.0000e-10
ti 316401 org Escherichia_coli_ETEC_H10407	MiSeq	1.00000e-10	8.00000e-10	0.0000e+00

Frequency a specific contaminant was observed in a dataset

```
ggplot(df[df$Contam == TRUE & df$Genome %in% df_contam$Genome[df_contam$median > 1e-10],]) + geom_raster(aes(x = sampleID, y = Genome, Fill=Final_Best_Hit_Read_Numbers)) + facet_wrap(~plat, scale= "free_x")
```



Need to filter out Genomes only present in one dataset and order by number of replicates present

Summary by org

```
df_summary <- ddply(df,.variables = .(Genome, plat),summarize, median=median(Final_Guess), max=max(Final_Guess),min=min(Final_Guess)) %>% arrange(desc(median))
```

Genome	plat	median	max	min
ti 99287 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str._LT2	PGM	0.9989104	0.9994742	0.9974006
ti 216597 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str._SL1344	MiSeq	0.9580343	0.9595847	0.9561871
ti 99287 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str._LT2	MiSeq	0.0375543	0.0383811	0.0369952
ti 1081093 org Salmonella_enterica_subsp.entericaserovar_Gallinarum/pullorum	MiSeq	0.0021782	0.0033778	0.0015996
ti 718274 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str.	PGM	0.0009326	0.0021647	0.0000000
ti 718274 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str.	MiSeq	0.0007477	0.0010610	0.0004312
ti 439851 org Salmonella_enterica_subsp.entericaserovar_Dublin_str.CT02021853	MiSeq	0.0005894	0.0007940	0.0003154
ti 1171376 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str._U288	PGM	0.0005691	0.0025988	0.0000000
ti 605 org Salmonella_enterica_subsp.entericaserovar_Pullorum	MiSeq	0.0001644	0.0002526	0.0001093
ti 990282 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str._UK-1	MiSeq	0.0001632	0.0002754	0.0000292
ti 1171376 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str._U288	MiSeq	0.0001345	0.0002515	0.0000462
ti 90371 org Salmonella_enterica_subsp.entericaserovar_Typhimurium	MiSeq	0.0001081	0.0001500	0.0000338
ti 568708 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str._D23580	MiSeq	0.0000690	0.0001659	0.0000400
ti 909946 org Salmonella_enterica_subsp.entericaserovar_Typhimurium_str._ST4/74	MiSeq	0.0000216	0.0000581	0.0000006
ti 454169 org Salmonella_enterica_subsp.entericaserovar_Heidelberg_str._SL476	MiSeq	0.0000192	0.0000554	0.0000055
ti 439843 org Salmonella_enterica_subsp.entericaserovar_Schwarzengrund_str.	MiSeq	0.0000155	0.0000279	0.0000000

ti 1016998 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Paratyphi_B_str._SPB7	MiSeq 0.0000146 0.0000243 0.0000034
ti 32630 org synthetic_construct	MiSeq 0.0000112 0.0000304 0.0000000
ti 149539 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Enteritidis	MiSeq 0.0000096 0.0000291 0.0000007
ti 696406 org Escherichia_coli_UMNK88	MiSeq 0.0000059 0.0000059 0.0000059
ti 476213 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Paratyphi_C_strain	MiSeq 0.0000049 0.0000086 0.0000003
ti 1267753 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Javiana_str.	MiSeq 0.0000042 0.0000095 0.0000009
ti 481805 org Escherichia_coli_ATCC_8739	MiSeq 0.0000038 0.0000079 0.0000001
ti 300268 org Shigella_boydii_Sb227	MiSeq 0.0000025 0.0000025 0.0000025
ti 117541 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Ohio	MiSeq 0.0000019 0.0000019 0.0000019
ti 554290 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Paratyphi_A_str.	MiSeq 0.0000019 0.0000031 0.0000007
ti 1008297 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhimurium_str._798	MiSeq 0.0000017 0.0000026 0.0000000
ti 59246 org Salmonella_enterica_VI_1,6,14,25:a:e,n,x	MiSeq 0.0000016 0.0000033 0.0000000
ti 295319 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Paratyphi_A_str._ATCC	MiSeq 0.0000010 0.0000088 0.0000000
ti 454166 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Agona_str._SL483	MiSeq 0.0000010 0.0000109 0.0000000
ti 585055 org Escherichia_coli_55989	PGM 0.0000009 0.0000019 0.0000000
ti 220341 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhi_str._CT18	MiSeq 0.0000009 0.0000056 0.0000000
ti 321314 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Choleraesuis_str.	MiSeq 0.0000009 0.0000071 0.0000001
ti 28147 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Oranienburg	MiSeq 0.0000009 0.0000017 0.0000000
ti 41514 org Salmonella_enterica_subsp. <i>arizona</i> serovar_62:z4,z23:-	MiSeq 0.0000007 0.0000041 0.0000002
ti 527001 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhi_str._Ty21a	MiSeq 0.0000007 0.0000013 0.0000000
ti 536056 org Escherichia_coli_DH1	PGM 0.0000007 0.0000051 0.0000000
ti 550537 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Enteritidis_str.	MiSeq 0.0000006 0.0000030 0.0000000
ti 1246486 org synthetic_Enterobacteria_phage_phiX174.1f	MiSeq 0.0000006 0.0000012 0.0000000
ti 936157 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Weltevreden_str.	MiSeq 0.0000006 0.0000042 0.0000001
ti 218493 org Salmonella_bongori_NCTC_12419	MiSeq 0.0000003 0.0000031 0.0000000
ti 266264 org Cupriavidus_metallidurans_CH34	MiSeq 0.0000003 0.0000003 0.0000003
ti 910348 org Escherichia_coli_P12b	MiSeq 0.0000003 0.0000118 0.0000000
ti 59244 org Salmonella_enterica_subsp. <i>houtena</i> serovar_43:z4,z23:-	MiSeq 0.0000003 0.0000003 0.0000003
ti 331112 org Escherichia_coli_HS	PGM 0.0000003 0.0000003 0.0000002
ti 1028764 org Cloning_vector_HPdO	MiSeq 0.0000003 0.0000005 0.0000000
ti 149387 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Brandenburg	MiSeq 0.0000002 0.0000002 0.0000002
ti 59201 org Salmonella_enterica_subsp._enterica	MiSeq 0.0000002 0.0000028 0.0000000
ti 858313 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Monteideo_str._414877	MiSeq 0.0000002 0.0000005 0.0000000
ti 1245786 org Salmonella_sp._CMCC50041	MiSeq 0.0000002 0.0000004 0.0000000
ti 550538 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Gallinarum_str._287/91	MiSeq 0.0000002 0.0000016 0.0000000
ti 423368 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Newport_str._SL254	MiSeq 0.0000002 0.0000044 0.0000000
ti 766762 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Monteideo_str.	MiSeq 0.0000002 0.0000006 0.0000000
ti 1160717 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Heidelberg_str._B182	MiSeq 0.0000002 0.0000046 0.0000000
ti 1218933 org Pectobacterium_carotovorum_subsp. <i>carotovorum</i> PCC21	MiSeq 0.0000001 0.0000003 0.0000000
ti 596 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Muenchen	MiSeq 0.0000001 0.0000001 0.0000001
ti 10847 org Enterobacteria_phage_phiX174	MiSeq 0.0000001 0.0000043 0.0000000
ti 1160730 org Salmonella_enterica_subsp. <i>enterica</i> serovar_1,4,(5),12:i:-	MiSeq 0.0000001 0.0000001 0.0000001
ti 274589 org VCSM13_interference-resistant_helper_phage	MiSeq 0.0000001 0.0000005 0.0000000
ti 0 org Unknown.	MiSeq 0.0000001 0.0000006 0.0000000
ti 693216 org Cronobacter_turicensis_z3032	MiSeq 0.0000001 0.0000001 0.0000001
ti 119912 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Choleraesuis	MiSeq 0.0000001 0.0000001 0.0000001
ti 28144 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Derby	MiSeq 0.0000001 0.0000001 0.0000001

ti 871588 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Montevideo_str.	MiSeq 0.0000001 0.0000001 0.0000001
ti 28901 org Salmonella_enterica	MiSeq 0.0000001 0.0000008 0.0000000
ti 585054 org Escherichia_fergusonii_ATCC_35469	MiSeq 0.0000001 0.0000001 0.0000000
ti 926017 org VCSM13_AviTag-pVII_modified_interference-resistant_helper_phage	MiSeq 0.0000001 0.0000001 0.0000000
ti 926018 org VCSM13_FLAG-pVII_modified_interference-resistant_helper_phage	MiSeq 0.0000001 0.0000001 0.0000000
ti 926019 org VCSM13_HIS6-pVII_modified_interference-resistant_helper_phage	MiSeq 0.0000001 0.0000001 0.0000000
ti 340190 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Schwarzengrund	MiSeq 0.0000001 0.0000001 0.0000001
ti 108619 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Newport	MiSeq 0.0000001 0.0000011 0.0000000
ti 1045856 org Enterobacter_cloacae_EcWSU1	MiSeq 0.0000001 0.0000001 0.0000000
ti 507522 org Klebsiella_pneumoniae_342	MiSeq 0.0000001 0.0000001 0.0000001
ti 511145 org Escherichia_coli_str.K-12substr._MG1655	MiSeq 0.0000000 0.0000000 0.0000000
ti 751903 org Human_artificial_chromosome_vector_21HAC4	MiSeq 0.0000000 0.0000000 0.0000000
ti 215689 org Erwinia_sp._Ejp617	MiSeq 0.0000000 0.0000002 0.0000000
ti 2341 org primary_endosymbiont_of_Sitophilus_zeamais	MiSeq 0.0000000 0.0000000 0.0000000
ti 536056 org Escherichia_coli_DH1	MiSeq 0.0000000 0.0000073 0.0000000
ti 98360 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Dublin	MiSeq 0.0000000 0.0000002 0.0000000
ti 10844 org Enterobacteria_phage_S13	MiSeq 0.0000000 0.0000000 0.0000000
ti 929814 org Salmonella_phage_RE-2010	MiSeq 0.0000000 0.0000001 0.0000000
ti 129861 org Phage_Gifsy-1	MiSeq 0.0000000 0.0000000 0.0000000
ti 439855 org Escherichia_coli_SMS-3-5	MiSeq 0.0000000 0.0000000 0.0000000
ti 550 org Enterobacter_cloacae	MiSeq 0.0000000 0.0000001 0.0000000
ti 362663 org Escherichia_coli_536	MiSeq 0.0000000 0.0000000 0.0000000
ti 544404 org Escherichia_coli_O157:H7_str._TW14359	MiSeq 0.0000000 0.0000000 0.0000000
ti 57046 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Paratyphi_C	MiSeq 0.0000000 0.0000001 0.0000000
ti 1132507 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhi_str._P-stx-12	MiSeq 0.0000000 0.0000009 0.0000000
ti 378823 org cotton_phyllosphere_bacterium_L	MiSeq 0.0000000 0.0000000 0.0000000
ti 29472 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Panama	MiSeq 0.0000000 0.0000001 0.0000000
ti 1125630 org Klebsiella_pneumoniae_subsp. <i>pneumoniae</i> HS11286	MiSeq 0.0000000 0.0000002 0.0000000
ti 153591 org Cloning_vector_HO-hisG-URA3-hisG-poly-HO	MiSeq 0.0000000 0.0000000 0.0000000
ti 486998 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Litchfield	MiSeq 0.0000000 0.0000000 0.0000000
ti 858316 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Montevideo_str._446600	MiSeq 0.0000000 0.0000000 0.0000000
ti 866789 org Escherichia_coli_DSM_30083_= <i>JCM</i> 1649	MiSeq 0.0000000 0.0000001 0.0000000
ti 199310 org Escherichia_coli_CFT073	MiSeq 0.0000000 0.0000000 0.0000000
ti 701347 org Enterobacter_cloacae_SCF1	MiSeq 0.0000000 0.0000000 0.0000000
ti 1211025 org Enterobacter_cloacae_subsp. <i>cloacae</i> ENHKU01	MiSeq 0.0000000 0.0000001 0.0000000
ti 134047 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Bredeney	MiSeq 0.0000000 0.0000000 0.0000000
ti 59208 org Salmonella_enterica_subsp._VII	MiSeq 0.0000000 0.0000000 0.0000000
ti 399281 org Salmonella_sp. <i>ICMP</i> 15669	MiSeq 0.0000000 0.0000000 0.0000000
ti 46629 org Salmonella_enterica_subsp. <i>salamae</i> serovar_Sofia	MiSeq 0.0000000 0.0000000 0.0000000
ti 90370 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhi	MiSeq 0.0000000 0.0000009 0.0000000
ti 693444 org Enterobacteriaceae_bacterium_strain_FGI_57	MiSeq 0.0000000 0.0000002 0.0000000
ti 956149 org Cronobacter_sakazakii_SP291	MiSeq 0.0000000 0.0000000 0.0000000
ti 440524 org Salmonella_enterica_subsp. <i>enterica</i> serovar_4,[5],12:i:-	MiSeq 0.0000000 0.0000000 0.0000000
ti 749949 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Montevideo_str.	MiSeq 0.0000000 0.0000000 0.0000000
ti 1191061 org Klebsiella_oxytoca_E718	MiSeq 0.0000000 0.0000000 0.0000000
ti 57045 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Paratyphi_B	MiSeq 0.0000000 0.0000005 0.0000000
ti 611 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Heidelberg	MiSeq 0.0000000 0.0000000 0.0000000

ti 644 org Aeromonas_hydrophila	MiSeq 0.0000000 0.0000005 0.0000000
ti 155900 org uncultured_organism	MiSeq 0.0000000 0.0000000 0.0000000
ti 59202 org Salmonella_enterica_subsp._salamae	MiSeq 0.0000000 0.0000000 0.0000000
ti 42897 org Shigella_flexneri_2a	MiSeq 0.0000000 0.0000000 0.0000000
ti 9606 org Homo_sapiens	PGM 0.0000000 0.0000000 0.0000000
ti 28150 org Salmonella_enterica_subsp. <i>entericasero</i> var_Senftenberg	MiSeq 0.0000000 0.0000001 0.0000000
ti 568095 org Salmonella_enterica_subsp. <i>entericasero</i> var_Hartford	MiSeq 0.0000000 0.0000000 0.0000000
ti 399742 org Enterobacter_sp._638	MiSeq 0.0000000 0.0000000 0.0000000
ti 858315 org Salmonella_enterica_subsp. <i>entericasero</i> var_Montevideo_str._413180	MiSeq 0.0000000 0.0000000 0.0000000
ti 935296 org Enterobacter_aerogenes_EA1509E	MiSeq 0.0000000 0.0000000 0.0000000
ti 515309 org Cloning_vector_pMQ118	MiSeq 0.0000000 0.0000000 0.0000000
ti 515316 org Cloning_vector_pMQ150	MiSeq 0.0000000 0.0000000 0.0000000
ti 651991 org Allelic_replacement_vector_pMQ236	MiSeq 0.0000000 0.0000000 0.0000000
ti 484021 org Klebsiella_pneumoniae_subsp. <i>pneumoniae</i> NTUH-K2044	MiSeq 0.0000000 0.0000000 0.0000000
ti 637910 org Citrobacter_rodentium_ICC168	MiSeq 0.0000000 0.0000003 0.0000000
ti 594 org Salmonella_enterica_subsp. <i>entericasero</i> var_Gallinarum	MiSeq 0.0000000 0.0000000 0.0000000
ti 284011 org uncultured_Klebsiella_sp.	MiSeq 0.0000000 0.0000000 0.0000000
ti 858318 org Salmonella_enterica_subsp. <i>entericasero</i> var_Montevideo_str.	MiSeq 0.0000000 0.0000000 0.0000000
ti 585396 org Escherichia_coli_O111:H-str.11128	MiSeq 0.0000000 0.0000000 0.0000000
ti 1204530 org Salmonella_phage_STML-13-1	MiSeq 0.0000000 0.0000000 0.0000000
ti 592316 org Pantoea_sp._At-9b	MiSeq 0.0000000 0.0000000 0.0000000
ti 260677 org Salmonella_enterica_subsp. <i>entericasero</i> var_Urbana	MiSeq 0.0000000 0.0000000 0.0000000
ti 398578 org Delftia_acidovorans_SPH-1	MiSeq 0.0000000 0.0000000 0.0000000
ti 373384 org Shigella_flexneri_5_str._8401	MiSeq 0.0000000 0.0000000 0.0000000
ti 1166130 org Enterobacter_sp._R4-368	MiSeq 0.0000000 0.0000000 0.0000000
ti 57741 org Salmonella_enterica_subsp. <i>entericasero</i> var_Blockley	MiSeq 0.0000000 0.0000000 0.0000000
ti 77133 org uncultured_bacterium	MiSeq 0.0000000 0.0000070 0.0000000
ti 59207 org Salmonella_enterica_subsp._indica	MiSeq 0.0000000 0.0000000 0.0000000
ti 300269 org Shigella_sonnei_Ss046	MiSeq 0.0000000 0.0000000 0.0000000
ti 562 org Escherichia_coli	MiSeq 0.0000000 0.0000023 0.0000000
ti 585397 org Escherichia_coli_ED1a	MiSeq 0.0000000 0.0000058 0.0000000
ti 192953 org Salmonella_enterica_subsp. <i>entericasero</i> var_Stanley	MiSeq 0.0000000 0.0000000 0.0000000
ti 716541 org Enterobacter_cloacae_subsp. <i>cloacae</i> ATCC_13047	MiSeq 0.0000000 0.0000003 0.0000000
ti 1028307 org Enterobacter_aerogenes_KCTC_2190	MiSeq 0.0000000 0.0000000 0.0000000
ti 630626 org Shimwellia_blattae_DSM_4481_= <i>NBRC</i> 105725	MiSeq 0.0000000 0.0000000 0.0000000
ti 1104326 org Enterobacter_cloacae_subsp. <i>dissolvens</i> SDM	MiSeq 0.0000000 0.0000000 0.0000000
ti 59204 org Salmonella_enterica_subsp._diarizonae	MiSeq 0.0000000 0.0000000 0.0000000
ti 6999 org Gryllus_bimaculatus	MiSeq 0.0000000 0.0000000 0.0000000
ti 360102 org Yersinia_pestis_Antiqua	MiSeq 0.0000000 0.0000000 0.0000000
ti 290338 org Citrobacter_koseri_ATCC_BAA-895	MiSeq 0.0000000 0.0000001 0.0000000
ti 548 org Enterobacter_aerogenes	MiSeq 0.0000000 0.0000000 0.0000000
ti 436295 org Salmonella_enterica_subsp. <i>entericasero</i> var_Poona	MiSeq 0.0000000 0.0000000 0.0000000
ti 209261 org Salmonella_enterica_subsp. <i>entericasero</i> var_Typhi_str._Ty2	MiSeq 0.0000000 0.0000007 0.0000000
ti 405955 org Escherichia_coli_APEC_O1	MiSeq 0.0000000 0.0000000 0.0000000
ti 198628 org Dickeya_dadantii_3937	MiSeq 0.0000000 0.0000000 0.0000000
ti 869729 org Escherichia_coli_UM146	MiSeq 0.0000000 0.0000000 0.0000000
ti 181736 org Salmonella_enterica_subsp. <i>entericasero</i> var_Schleissheim	MiSeq 0.0000000 0.0000000 0.0000000

ti 716540 org Erwinia_amylovora_ATCC_49946	MiSeq 0.0000000 0.0000000 0.0000000
ti 640131 org Klebsiella_variicola_At-22	MiSeq 0.0000000 0.0000000 0.0000000
ti 32630 org synthetic_construct	PGM 0.0000000 0.0000002 0.0000000
ti 235565 org Arsenophonus_endosymbiont_of_Tetraleurodes_acaciae	MiSeq 0.0000000 0.0000000 0.0000000
ti 198215 org Shigella_flexneri_2a_str._2457T	MiSeq 0.0000000 0.0000000 0.0000000
ti 703 org Plesiomonas_shigelloides	MiSeq 0.0000000 0.0000000 0.0000000
ti 655817 org Escherichia_coli_ABU_83972	MiSeq 0.0000000 0.0000000 0.0000000
ti 431946 org Escherichia_coli_SE15	MiSeq 0.0000000 0.0000000 0.0000000
ti 358220 org Acidovorax_sp._KKS102	MiSeq 0.0000000 0.0000000 0.0000000
ti 1095774 org Pantoea_ananatis_PA13	MiSeq 0.0000000 0.0000000 0.0000000
ti 96563 org Pseudomonas_stutzeri_ATCC_17588_=LMG11199	MiSeq 0.0000000 0.0000000 0.0000000
ti 444450 org Escherichia_coli_O157:H7_str._EC4115	MiSeq 0.0000000 0.0000000 0.0000000
ti 59203 org Salmonella_enterica_subsp._arizonae	MiSeq 0.0000000 0.0000000 0.0000000
ti 1005996 org Raoultella_planticola_ATCC_33531	MiSeq 0.0000000 0.0000000 0.0000000
ti 59205 org Salmonella_enterica_subsp._houtenae	MiSeq 0.0000000 0.0000000 0.0000000
ti 386656 org Yersinia_pestis_Pestoides_F	MiSeq 0.0000000 0.0000000 0.0000000
ti 469008 org Escherichia_coli_BL21(DE3)	MiSeq 0.0000000 0.0000000 0.0000000
ti 316401 org Escherichia_coli_ETEC_H10407	MiSeq 0.0000000 0.0000000 0.0000000
ti 573 org Klebsiella_pneumoniae	MiSeq 0.0000000 0.0000001 0.0000000
ti 615 org Serratia_marcescens	MiSeq 0.0000000 0.0000000 0.0000000
ti 519 org Bordetella_parapertussis	MiSeq 0.0000000 0.0000000 0.0000000
ti 640513 org Enterobacter_asburiae_LF7a	MiSeq 0.0000000 0.0000000 0.0000000
ti 871585 org Acinetobacter_calcoaceticus_PHEA-2	PGM 0.0000000 0.0000000 0.0000000
ti 634503 org Edwardsiella_ictaluri_93-146	MiSeq 0.0000000 0.0000000 0.0000000
ti 272776 org Arsenophonus_endosymbiont_of_Trialeurodes_hutchingsi	MiSeq 0.0000000 0.0000000 0.0000000
ti 634500 org Erwinia_billingiae_Eb661	MiSeq 0.0000000 0.0000000 0.0000000
ti 54388 org Salmonella_enterica_subsp._entericaserovar_Paratyphi_A	MiSeq 0.0000000 0.0000000 0.0000000
ti 85643 org Thauera_sp._MZ1T	MiSeq 0.0000000 0.0000000 0.0000000
ti 331111 org Escherichia_coli_E24377A	MiSeq 0.0000000 0.0000003 0.0000000
ti 61648 org Kluyvera_intermedia	MiSeq 0.0000000 0.0000000 0.0000000
ti 1193292 org Klebsiella_pneumoniae_subsp._pneumoniae1084	MiSeq 0.0000000 0.0000000 0.0000000
ti 665029 org Erwinia_amylovora_CFBP1430	MiSeq 0.0000000 0.0000000 0.0000000
ti 868597 org Stenotrophomonas_maltophilia_JV3	PGM 0.0000000 0.0000000 0.0000000
ti 1006551 org Klebsiella_oxytoca_KCTC_1686	MiSeq 0.0000000 0.0000000 0.0000000
ti 561229 org Dickeya_zeae_Ech1591	MiSeq 0.0000000 0.0000000 0.0000000
ti 571 org Klebsiella_oxytoca	MiSeq 0.0000000 0.0000000 0.0000000
ti 35703 org Citrobacter_amalonaticus	MiSeq 0.0000000 0.0000000 0.0000000
ti 10090 org Mus_musculus	MiSeq 0.0000000 0.0000000 0.0000000
ti 149385 org Salmonella_enterica_subsp._entericaserovar_Hadar	MiSeq 0.0000000 0.0000001 0.0000000
ti 633149 org Brevundimonas_subvibrioides_ATCC_15264	MiSeq 0.0000000 0.0000000 0.0000000
ti 546 org Citrobacter_freundii	MiSeq 0.0000000 0.0000000 0.0000000
ti 547628 org Enterobacter_sp._ECC120	MiSeq 0.0000000 0.0000000 0.0000000
ti 868597 org Stenotrophomonas_maltophilia_JV3	MiSeq 0.0000000 0.0000000 0.0000000
ti 1124991 org Morganella_morganii_subsp._morganiiKT	MiSeq 0.0000000 0.0000002 0.0000000
ti 192955 org Salmonella_enterica_subsp._entericaserovar_Kentucky	MiSeq 0.0000000 0.0000000 0.0000000
ti 742013 org Delftia_sp._Cs1-4	MiSeq 0.0000000 0.0000000 0.0000000
ti 1123863 org Pantoea_ananatis_LMG_5342	MiSeq 0.0000000 0.0000000 0.0000000

ti 1027360 org Edwardsiella_ictaluri_ATCC_33202	MiSeq 0.0000000 0.0000000 0.0000000
ti 596154 org Alicyclophilus_denitrificans_K601	MiSeq 0.0000000 0.0000000 0.0000000
ti 386585 org Escherichia_coli_O157:H7_str._Sakai	MiSeq 0.0000000 0.0000000 0.0000000
ti 1037911 org Pseudomonas_fluorescens_A506	MiSeq 0.0000000 0.0000045 0.0000000
ti 300267 org Shigella_dysenteriae_Sd197	MiSeq 0.0000000 0.0000000 0.0000000
ti 545 org Citrobacter_koseri	MiSeq 0.0000000 0.0000000 0.0000000
ti 1196835 org Pseudomonas_stutzeri_CCUG_29243	PGM 0.0000000 0.0000000 0.0000000
ti 1286170 org Raoultella_ornithinolytica_B6	MiSeq 0.0000000 0.0000000 0.0000000
ti 28141 org Cronobacter_sakazakii	MiSeq 0.0000000 0.0000001 0.0000000
ti 263771 org uncultured_Salmonella_sp.	MiSeq 0.0000000 0.0000000 0.0000000
ti 1072459 org Escherichia_coli_O7:K1_str._CE10	MiSeq 0.0000000 0.0000000 0.0000000
ti 1167634 org Achromobacter_xylosoxidans_NH44784-1996	MiSeq 0.0000000 0.0000000 0.0000000
ti 593904 org Salmonella_enterica_subsp.entericasero var_Amsterdam	MiSeq 0.0000000 0.0000000 0.0000000
ti 208962 org Escherichia_albertii	MiSeq 0.0000000 0.0000000 0.0000000
ti 398578 org Delftia_acidovorans_SPH-1	PGM 0.0000000 0.0000000 0.0000000
ti 1163399 org Stenotrophomonas_maltophilia_D457	MiSeq 0.0000000 0.0000000 0.0000000
ti 1208658 org Bordetella_bronchiseptica_MO149	PGM 0.0000000 0.0000000 0.0000000
ti 977880 org Cupriavidus_taiwanensis_LMG_19424	PGM 0.0000000 0.0000000 0.0000000
ti 288000 org Bradyrhizobium_sp._BTai1	PGM 0.0000000 0.0000000 0.0000000
ti 509190 org Caulobacter_segnis_ATCC_21756	MiSeq 0.0000000 0.0000000 0.0000000
ti 1037911 org Pseudomonas_fluorescens_A506	PGM 0.0000000 0.0000000 0.0000000
ti 861208 org Agrobacterium_sp._H13-3	MiSeq 0.0000000 0.0000000 0.0000000
ti 243265 org Photorhabdus_luminescens_subsp.laumondiiTTO1	MiSeq 0.0000000 0.0000000 0.0000000
ti 549 org Pantoea_agglomerans	MiSeq 0.0000000 0.0000000 0.0000000
ti 440085 org Methylobacterium_extorquens_CM4	PGM 0.0000000 0.0000000 0.0000000
ti 454169 org Salmonella_enterica_subsp.entericasero var_Heidelberg_str._SL476	PGM 0.0000000 0.0000000 0.0000000
ti 1163399 org Stenotrophomonas_maltophilia_D457	PGM 0.0000000 0.0000000 0.0000000
ti 266264 org Cupriavidus_metallidurans_CH34	PGM 0.0000000 0.0000000 0.0000000
ti 754307 org Escherichia_sp._B1147	MiSeq 0.0000000 0.0000000 0.0000000
ti 465817 org Erwinia_tasmaniensis_Et1/99	MiSeq 0.0000000 0.0000000 0.0000000
ti 1331671 org Pseudomonas_putida_H8234	MiSeq 0.0000000 0.0000000 0.0000000
ti 522373 org Stenotrophomonas_maltophilia_K279a	PGM 0.0000000 0.0000000 0.0000000
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ti 1001585 org Pseudomonas_mendocina_NK-01	PGM 0.0000000 0.0000000 0.0000000
ti 391008 org Stenotrophomonas_maltophilia_R551-3	PGM 0.0000000 0.0000000 0.0000000
ti 232721 org Acidovorax_sp._JS42	MiSeq 0.0000000 0.0000000 0.0000000
ti 590161 org Origami_vector_p7704	MiSeq 0.0000000 0.0000000 0.0000000
ti 393305 org Yersinia_enterocolitica_subsp.enterocolitica8081	MiSeq 0.0000000 0.0000000 0.0000000
ti 441620 org Methylobacterium_populi_BJ001	PGM 0.0000000 0.0000000 0.0000000
ti 419610 org Methylobacterium_extorquens_PA1	MiSeq 0.0000000 0.0000000 0.0000000
ti 441620 org Methylobacterium_populi_BJ001	MiSeq 0.0000000 0.0000000 0.0000000
ti 234621 org Rhodococcus_erythropolis_PR4	PGM 0.0000000 0.0000000 0.0000000
ti 454166 org Salmonella_enterica_subsp.entericasero var_Agona_str._SL483	PGM 0.0000000 0.0000000 0.0000000
ti 661410 org Methylobacterium_extorquens_DM4	MiSeq 0.0000000 0.0000000 0.0000000
ti 7176 org Culex_quinquefasciatus	MiSeq 0.0000000 0.0000000 0.0000000
ti 588858 org Salmonella_enterica_subsp.entericasero var_Typhimurium_str._14028S	PGM 0.0000000 0.0000000 0.0000000
ti 234621 org Rhodococcus_erythropolis_PR4	MiSeq 0.0000000 0.0000000 0.0000000

ti 1167634 org Achromobacter_xylosoxidans_NH44784-1996	PGM	0.0000000	0.0000000	0.0000000
ti 871585 org Acinetobacter_calcoaceticus_PHEA-2	MiSeq	0.0000000	0.0000000	0.0000000
ti 391008 org Stenotrophomonas_maltophilia_R551-3	MiSeq	0.0000000	0.0000002	0.0000000
ti 861208 org Agrobacterium_sp._H13-3	PGM	0.0000000	0.0000000	0.0000000
ti 440085 org Methylobacterium_extorquens_CM4	MiSeq	0.0000000	0.0000000	0.0000000
ti 331111 org Escherichia_coli_E24377A	PGM	0.0000000	0.0000000	0.0000000
ti 630 org Yersinia_enterocolitica	MiSeq	0.0000000	0.0000000	0.0000000
ti 605 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Pullorum	PGM	0.0000000	0.0000000	0.0000000
ti 9606 org Homo_sapiens	MiSeq	0.0000000	0.0000000	0.0000000
ti 550537 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Enteritidis_str.	PGM	0.0000000	0.0000000	0.0000000
ti 990282 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhimurium_str._UK-1	PGM	0.0000000	0.0000000	0.0000000
ti 661410 org Methylobacterium_extorquens_DM4	PGM	0.0000000	0.0000000	0.0000000
ti 585056 org Escherichia_coli_UMN026	MiSeq	0.0000000	0.0000000	0.0000000
ti 909946 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhimurium_str._ST4/74	PGM	0.0000000	0.0000000	0.0000000
ti 6183 org Schistosoma_mansoni	MiSeq	0.0000000	0.0000000	0.0000000
ti 4577 org Zea_mays	MiSeq	0.0000000	0.0000000	0.0000000
ti 977880 org Cupriavidus_taiwanensis_LMG_19424	MiSeq	0.0000000	0.0000000	0.0000000
ti 40559 org Botryotinia_fuckeliana	MiSeq	0.0000000	0.0000000	0.0000000
ti 1305998 org fungal_sp._JF57	MiSeq	0.0000000	0.0000000	0.0000000
ti 6945 org Ixodes_scapularis	MiSeq	0.0000000	0.0000000	0.0000000
ti 585397 org Escherichia_coli_ED1a	PGM	0.0000000	0.0000000	0.0000000
ti 272630 org Methylobacterium_extorquens_AM1	MiSeq	0.0000000	0.0000000	0.0000000
ti 476213 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Paratyphi_C_strain	PGM	0.0000000	0.0000000	0.0000000
ti 595496 org Escherichia_coli_BW2952	PGM	0.0000000	0.0000000	0.0000000
ti 1008297 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhimurium_str._798	PGM	0.0000000	0.0000000	0.0000000
ti 568708 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhimurium_str._D23580	PGM	0.0000000	0.0000000	0.0000000
ti 1132507 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhi_str._P-stx-12	PGM	0.0000000	0.0000000	0.0000000
ti 90370 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhi	PGM	0.0000000	0.0000000	0.0000000
ti 321314 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Choleraesuis_str.	PGM	0.0000000	0.0000000	0.0000000
ti 1267753 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Javiana_str.	PGM	0.0000000	0.0000000	0.0000000
ti 423368 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Newport_str._SL254	PGM	0.0000000	0.0000000	0.0000000
ti 439843 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Schwarzengrund_str.	PGM	0.0000000	0.0000000	0.0000000
ti 439851 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Dublin_str.CT02021853	PGM	0.0000000	0.0000000	0.0000000
ti 119912 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Choleraesuis	PGM	0.0000000	0.0000000	0.0000000
ti 175950 org Salmonella_phage_ST64B	PGM	0.0000000	0.0000000	0.0000000
ti 220341 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhi_str._CT18	PGM	0.0000000	0.0000000	0.0000000
ti 956149 org Cronobacter_sakazakii_SP291	PGM	0.0000000	0.0000000	0.0000000
ti 59201 org Salmonella_enterica_subsp._enterica	PGM	0.0000000	0.0000000	0.0000000
ti 550538 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Gallinarum_str._287/91	PGM	0.0000000	0.0000000	0.0000000
ti 90371 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhimurium	PGM	0.0000000	0.0000003	0.0000000
ti 1081093 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Gallinarum/pullorum	PGM	0.0000000	0.0000000	0.0000000
ti 314565 org Xanthomonas_campestris_pv. <i>campestris</i> str._8004	MiSeq	0.0000000	0.0000000	0.0000000
ti 218493 org Salmonella_bongori_NCTC_12419	PGM	0.0000000	0.0000000	0.0000000
ti 554290 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Paratyphi_A_str.	PGM	0.0000000	0.0000000	0.0000000
ti 1160717 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Heidelberg_str._B182	PGM	0.0000000	0.0000000	0.0000000
ti 77133 org uncultured_bacterium	PGM	0.0000000	0.0000000	0.0000000
ti 209261 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Typhi_str._Ty2	PGM	0.0000000	0.0000000	0.0000000

ti 936157 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Weltevreden_str.	PGM	0.0000000	0.0000000	0.0000000
ti 595495 org Escherichia_coli_KO11FL	PGM	0.0000000	0.0000000	0.0000000
ti 718254 org Enterobacter_cloacae_subsp. <i>cloacae</i> NCTC_9394	PGM	0.0000000	0.0000000	0.0000000
ti 108619 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Newport	PGM	0.0000000	0.0000000	0.0000000
ti 1016998 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Paratyphi_B_str._SPB7	PGM	0.0000000	0.0000000	0.0000000
ti 46629 org Salmonella_enterica_subsp. <i>salamae</i> serovar_Sofia	PGM	0.0000000	0.0000000	0.0000000
ti 693216 org Cronobacter_turicensis_z3032	PGM	0.0000000	0.0000000	0.0000000
ti 28901 org Salmonella_enterica	PGM	0.0000000	0.0000000	0.0000000
ti 58096 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Bareilly	PGM	0.0000000	0.0000000	0.0000000
ti 41514 org Salmonella_enterica_subsp. <i>arizonae</i> serovar_62:z4,z23:-	PGM	0.0000000	0.0000000	0.0000000
ti 344609 org Shigella_boydii_CDC_3083-94	PGM	0.0000000	0.0000000	0.0000000
ti 1160769 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Worthington	PGM	0.0000000	0.0000000	0.0000000
ti 218034 org uncultured_Enterobacteriaceae_bacterium	PGM	0.0000000	0.0000000	0.0000000
ti 562 org Escherichia_coli	PGM	0.0000000	0.0000000	0.0000000
ti 529507 org Proteus_mirabilis_HI4320	PGM	0.0000000	0.0000000	0.0000000
ti 243277 org Vibrio_cholerae_O1_biovar_EI_Tor_str._N16961	PGM	0.0000000	0.0000000	0.0000000
ti 585054 org Escherichia_fergusonii_ATCC_35469	PGM	0.0000000	0.0000000	0.0000000
ti 290338 org Citrobacter_koseri_ATCC_BAA-895	PGM	0.0000000	0.0000000	0.0000000
ti 98360 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Dublin	PGM	0.0000000	0.0000000	0.0000000
ti 550540 org Ferrimonas_balearica_DSM_9799	PGM	0.0000000	0.0000000	0.0000000
ti 215689 org Erwinia_sp._Ejp617	PGM	0.0000000	0.0000000	0.0000000
ti 192955 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Kentucky	PGM	0.0000000	0.0000000	0.0000000
ti 316401 org Escherichia_coli_ETEC_H10407	PGM	0.0000000	0.0000000	0.0000000
ti 592316 org Pantoea_sp._At-9b	PGM	0.0000000	0.0000000	0.0000000
ti 1160750 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Istanbul	PGM	0.0000000	0.0000000	0.0000000
ti 712898 org Pantoea_vagans_C9-1	PGM	0.0000000	0.0000000	0.0000000
ti 6999 org Gryllus_bimaculatus	PGM	0.0000000	0.0000000	0.0000000
ti 315612 org Klebsiella_sp._7C	PGM	0.0000000	0.0000000	0.0000000
ti 637910 org Citrobacter_rodentium_ICC168	PGM	0.0000000	0.0000000	0.0000000
ti 218491 org Pectobacterium_atrosepticum_SCRI1043	PGM	0.0000000	0.0000000	0.0000000
ti 1104326 org Enterobacter_cloacae_subsp. <i>dissolvens</i> SDM	PGM	0.0000000	0.0000000	0.0000000
ti 286134 org uncultured_Shigella_sp.	PGM	0.0000000	0.0000000	0.0000000
ti 9823 org Sus_scrofa	PGM	0.0000000	0.0000000	0.0000000
ti 452662 org Sphingobium_japonicum_UT26S	MiSeq	0.0000000	0.0000000	0.0000000
ti 869729 org Escherichia_coli_UM146	PGM	0.0000000	0.0000000	0.0000000
ti 484021 org Klebsiella_pneumoniae_subsp. <i>pneumoniae</i> NTUH-K2044	PGM	0.0000000	0.0000000	0.0000000
ti 115981 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Montevideo	PGM	0.0000000	0.0000000	0.0000000
ti 1286170 org Raoultella_ornithinolytica_B6	PGM	0.0000000	0.0000000	0.0000000
ti 379731 org Pseudomonas_stutzeri_A1501	PGM	0.0000000	0.0000000	0.0000000
ti 64518 org Mortierella_alpina	MiSeq	0.0000000	0.0000000	0.0000000
ti 716541 org Enterobacter_cloacae_subsp. <i>cloacae</i> ATCC_13047	PGM	0.0000000	0.0000000	0.0000000
ti 28147 org Salmonella_enterica_subsp. <i>enterica</i> serovar_Oranienburg	PGM	0.0000000	0.0000000	0.0000000
ti 640512 org Burkholderia_sp._CCGE1003	MiSeq	0.0000000	0.0000000	0.0000000